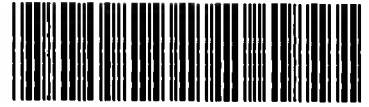DT15 Rec'd PCT/PTO N 2 4 2002

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PATENT APPLICATION: US/09/011,307

DATE: 06/04/2002   MAR 0 5 2004
TIME: 14:54:03

TECH CENTER 1600/2900

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SEQUENCE LISTING

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 4 (1) GENERAL INFORMATION:
 6       (i) APPLICANT: Zabeau, Marc
 7                     Vos, Pieter
 8                     Simons, Guus
10      (ii) TITLE OF INVENTION: RESISTANCE AGAINST WILT INDUCING FUNGI
12     (iii) NUMBER OF SEQUENCES: 12
14      (iv) CORRESPONDENCE ADDRESS:
15           (A) ADDRESSEE: SPENCER & FRANK
16           (B) STREET: 1100 New York Avenue, N.W., Suite 300 East
17           (C) CITY: Washington
18           (D) STATE: DC
19           (E) COUNTRY: USA
20           (F) ZIP: 20005
22       (v) COMPUTER READABLE FORM:
23           (A) MEDIUM TYPE: Floppy disk
24           (B) COMPUTER: IBM PC compatible
25           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26           (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
28      (vi) CURRENT APPLICATION DATA:
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C--> 29   (A) APPLICATION NUMBER: US/09/011,307
C--> 30   (B) FILING DATE: 01-Jul-1988

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31           (C) CLASSIFICATION:
33     (vii) PRIOR APPLICATION DATA:
34           (A) APPLICATION NUMBER: EP 95401849.5
35           (B) FILING DATE: 07-AUG-1995
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37    (viii) ATTORNEY/AGENT INFORMATION:
38           (A) NAME: Gollin, Michael A.
39           (B) REGISTRATION NUMBER: 31,957
40           (C) REFERENCE/DOCKET NUMBER: GUPLA 0008
42      (ix) TELECOMMUNICATION INFORMATION:
43           (A) TELEPHONE: 202-414-4000
44           (B) TELEFAX: 202-414-4040
47 (2) INFORMATION FOR SEQ ID NO: 1:
49       (i) SEQUENCE CHARACTERISTICS:
50           (A) LENGTH: 19 base pairs
51           (B) TYPE: nucleic acid
52           (C) STRANDEDNESS: single
53           (D) TOPOLOGY: linear
55      (ii) MOLECULE TYPE: other nucleic acid
56           (A) DESCRIPTION: /desc = "primer"
61      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
63 GACTGCGTAC CAATTCNNN                                              19
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PATENT APPLICATION: US/09/011,307

DATE: 06/04/2002
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Output Set: **N:\CRF3\06042002\I011307.raw**

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69          (B) TYPE: nucleic acid
70          (C) STRANDEDNESS: single
71          (D) TOPOLOGY: linear
73      (ii) MOLECULE TYPE: other nucleic acid
74          (A) DESCRIPTION: /desc = "primer"
79      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
81 GATGAGTCCT GAGTAANNN                                    19
83 (2) INFORMATION FOR SEQ ID NO: 3:
85      (i) SEQUENCE CHARACTERISTICS:
86          (A) LENGTH: 17 base pairs
87          (B) TYPE: nucleic acid
88          (C) STRANDEDNESS: single
89          (D) TOPOLOGY: linear
91      (ii) MOLECULE TYPE: other nucleic acid
92          (A) DESCRIPTION: /desc = "oligonucleotide"
97      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
99 CTCGTAGACT GCGTACC                                      17
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105          (B) TYPE: nucleic acid
106          (C) STRANDEDNESS: single
107          (D) TOPOLOGY: linear
109      (ii) MOLECULE TYPE: other nucleic acid
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117 AATTGGTACG CAGTCTAC                                    18
119 (2) INFORMATION FOR SEQ ID NO: 5:
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122          (A) LENGTH: 16 base pairs
123          (B) TYPE: nucleic acid
124          (C) STRANDEDNESS: single
125          (D) TOPOLOGY: linear
127      (ii) MOLECULE TYPE: other nucleic acid
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135 GACGATGAGT CCTGAG                                      16
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139      (i) SEQUENCE CHARACTERISTICS:
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RAW SEQUENCE LISTING   DATE: 06/04/2002
PATENT APPLICATION: US/09/011,307   TIME: 14:54:03

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159           (B) TYPE: nucleic acid
160           (C) STRANDEDNESS: single
161           (D) TOPOLOGY: linear
163     (ii) MOLECULE TYPE: other nucleic acid
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169     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
171 GACTGCGTAC CAATTC                                                  16
173 (2) INFORMATION FOR SEQ ID NO: 8:
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176           (A) LENGTH: 16 base pairs
177           (B) TYPE: nucleic acid
178           (C) STRANDEDNESS: single
179           (D) TOPOLOGY: linear
181     (ii) MOLECULE TYPE: other nucleic acid
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194           (A) LENGTH: 19 base pairs
195           (B) TYPE: nucleic acid
196           (C) STRANDEDNESS: single
197           (D) TOPOLOGY: linear
199     (ii) MOLECULE TYPE: other nucleic acid
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205     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
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209 (2) INFORMATION FOR SEQ ID NO: 10:
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212           (A) LENGTH: 19 base pairs
213           (B) TYPE: nucleic acid
214           (C) STRANDEDNESS: single
215           (D) TOPOLOGY: linear
217     (ii) MOLECULE TYPE: other nucleic acid
218           (A) DESCRIPTION: /desc = "primer"
223     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
225 GATGAGTCCT GAGTAATCT                                               19
227 (2) INFORMATION FOR SEQ ID NO: 11:
229      (i) SEQUENCE CHARACTERISTICS:
230           (A) LENGTH: 6658 base pairs
231           (B) TYPE: nucleic acid
232           (C) STRANDEDNESS: single
233           (D) TOPOLOGY: linear
235     (ii) MOLECULE TYPE: cDNA
238     (ix) FEATURE:
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239              (A) NAME/KEY: CDS
240              (B) LOCATION: 1798..5595
243     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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247 GCAGTTATGT GTTTGGAAWA AAAGTGCTGA AGTTGCTATG TCAAACATGA AAAGGGRAAA       120
249 AATGGAAGAA AGAGWTGTTA GGGTTATGTC GTAATTTGGA GATTGTATAA AAATATTAAG       180
251 GGCAAAAAAA ATAAAAATGT GTCAACTTAA AACAGCTTAT AAGCTAAAAG TTAAAAGCTG       240
253 GGGTAGAGGT GTTTTTTTTT TTTTTAGCTT ATAAGTTGTT TTAAGTTGAC CACATTTTTA       300
255 TTTTTKTTGC CCTTAATATT TTTATACAAT CTCAAAATTA CGACATAACC CTAACATCTT       360
257 TTTCTCCCAT TTTTTCCTTT TCACGTTTGA CATAGCAACT TCAGCACTTT TATCCAAACA       420
259 CATAACTGCT TATTTTAAAA ATAAGTTTCA GCACTTTCAA AAGTACTTTT TTAAAGCTGC       480
261 TTTTATTAAG CCCATCCAAA CGGGCCCTAA AATTGCTAAT GTTTGCTCTT TCTATTCTCA       540
263 AACTCCGTAA TATTTAAGAA AATTTGCTAA TGATAGGTCA CTTTTAACAC TAAATAATTA       600
265 TAAATTGGGT AGAAATTTAT TTATCATTTT AAGCTTTTTT AATTTTGAGT CTTCTCCCTA       660
267 ATTAAGACCC TTCCCCTCTT GCTTCAATTA TTTAACTGAA TAGTCTTTGT CTTATTGTTG       720
269 GGTGAAAGTC TGTCTTCTTG TTAGGTACTA AGTCCTACAA TAATATCAAT AATTTGCTAT       780
271 GGAGAAAAAA ATATTATAGG AGAAAAATAA TTAATTTTAA TTCATGAATA TGTCTTAATA       840
273 TGCAACTCAT TTTGCTTATA TATATCAAAT TAAACTCTGT TCCTTTAACT TTTTCCTATG       900
275 AAGATACATT TTAATTTATT TGATGAGGTT AGTTTTGAAA TTTATATTAT AATAATGAAA       960
277 TGATATAACT TAAAAGAAGT TGTTTGATAT CTTATCAGAA TCATGCAGGT ACTCATAATA      1020
279 TAAGAAATAA TTATGATGAA ATTTATATAT GTTTTATGCA GAGATTTATT ACGCATTGTT      1080
281 TACTTGGGTT ATGTATTACT TATTTCATCT TTTATCAGAA TGTAAAATTA TCATTCAATA      1140
283 AGAAATCCAA TTCTGTTAAA TTCAAAATAC AAACAATAAC ATTTTCAAGA CCGATTTTTT      1200
285 GCCCAAGAAT ATACAGTAAA CATATTTATG ATATGGTAGG TCTCTTTAGT AATTGACCAA      1260
287 CAAGGATTGT GGTGGAGTGG GAAATACTCT TTAATACTTC ACCAAGAGGT CTCCAATTTG      1320
289 AGCCCCTGAA TACGAAATCG TCTTTGTTAG TATATACCCT AACCTAATAC AAAAATTAGT      1380
291 ATATTAGCCT TNACAGCTAA AATCTTTGTG ACCTGTAAGT CACGCGAGGA CAAATTTACC      1440
293 GTAACACCAA CTTATTCATG ATATAATTGT CCCTTTTAGC ACGGTAATAA TGAGGTGGGT      1500
295 AGAAATTTAT TACTTGAGGG CCCTTTCTAC ACCCACCCTT ATTCTCTTGC TTCAATTATT      1560
297 GAATTGAAGA AGTAATGAAA AAACAGACTC CATTGGATAA AGGACAGTTT GCAAACACAG      1620
299 CTGTAACAAT TTAGAGCACT AGCAAAATAG AGAGAGTTTT GAGAGAAATT TTTGTTTGCA      1680
301 AATTACTCTT AACCTTCAGC AGGTAAAATA AAGTTCTTAA CTGAGACTAT TTGAAGATAT      1740
303 ATTTTGTTAA AGAATCATTT TGTGTGTTTC CTTGTTTTGC TTTTGCAGAT TTGAGAA        1797
305 ATG GAG ATT GGC TTA GCA GTT GGT GGT GCA TTT CTC TCC TCA GCT TTG      1845
306 Met Glu Ile Gly Leu Ala Val Gly Gly Ala Phe Leu Ser Ser Ala Leu
307  1               5                  10                  15
309 AAT GTT CTG TTT GAT AGG CTT GCT CCT AAC GGT GAT CTG CTC AAC ATG      1893
310 Asn Val Leu Phe Asp Arg Leu Ala Pro Asn Gly Asp Leu Leu Asn Met
311             20                  25                  30
313 TTT CGG AAG CAT AAG GAT CAT GTT AAG CTC TTA AAG AAG CTG AAA ATG      1941
314 Phe Arg Lys His Lys Asp His Val Lys Leu Leu Lys Lys Leu Lys Met
315         35                  40                  45
317 ACT TTG CGT GGT ATT CAG ATT GTG CTA AGT GAT GCA GAG AAT AAG CAA      1989
318 Thr Leu Arg Gly Ile Gln Ile Val Leu Ser Asp Ala Glu Asn Lys Gln
319   50                  55                  60
321 GCA TCA AAT CCA TCT GTG AGA GAC TGG CTT AAT GAG CTT CGA GAT GCT      2037
322 Ala Ser Asn Pro Ser Val Arg Asp Trp Leu Asn Glu Leu Arg Asp Ala
323 65                  70                  75                  80
325 GTC GAC TCT GCT GAA AAT TTA ATA GAA GAA GTC AAT TAT GAA GCT TTG      2085
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326 Val Asp Ser Ala Glu Asn Leu Ile Glu Glu Val Asn Tyr Glu Ala Leu
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330 Arg Leu Lys Val Glu Gly Gln His Gln Asn Phe Ser Glu Thr Ser Asn
331             100                     105                     110
333 CAG CAA GTA AGT GAT GAT TTT TTC CTT AAC ATA AAG GAC AAG CTG GAA        2181
334 Gln Gln Val Ser Asp Asp Phe Phe Leu Asn Ile Lys Asp Lys Leu Glu
335             115                     120                     125
337 GAC ACT ATT GAA ACA TTA AAG GAT TTG CAA GAG CAA ATT GGT CTC CTT        2229
338 Asp Thr Ile Glu Thr Leu Lys Asp Leu Gln Glu Gln Ile Gly Leu Leu
339         130                     135                     140
341 GGC TTA AAG GAG TAT TTT GAT TCC ACG AAA CTA GAA ACT AGA AGA CCT        2277
342 Gly Leu Lys Glu Tyr Phe Asp Ser Thr Lys Leu Glu Thr Arg Arg Pro
343 145                 150                     155                 160
345 TCA ACT TCT GTG GAT GAT GAA TCT GAT ATC TTT GGT AGG CAG AGC GAA        2325
346 Ser Thr Ser Val Asp Asp Glu Ser Asp Ile Phe Gly Arg Gln Ser Glu
347                 165                     170                     175
349 ATA GAG GAT TTG ATT GAC CGT CTA TTG TCT GAA GGT GCA AGT GGG AAA        2373
350 Ile Glu Asp Leu Ile Asp Arg Leu Leu Ser Glu Gly Ala Ser Gly Lys
351             180                     185                     190
353 AAG CTG ACA GTA GTT CCT ATC GTT GGA ATG GGC GGC CAG GGC AAG ACA        2421
354 Lys Leu Thr Val Val Pro Ile Val Gly Met Gly Gly Gln Gly Lys Thr
355             195                     200                     205
357 ACA CTT GCT AAA GCC GTA TAC AAT GAT GAG AGG GTG AAG AAT CAT TTT        2469
358 Thr Leu Ala Lys Ala Val Tyr Asn Asp Glu Arg Val Lys Asn His Phe
359         210                     215                     220
361 GAT TTG AAA GCG TGG TAT TGC GTT TCT GAA GGA TTT GAT GCT TTG AGA        2517
362 Asp Leu Lys Ala Trp Tyr Cys Val Ser Glu Gly Phe Asp Ala Leu Arg
363 225                 230                     235                 240
365 ATA ACA AAA GAA TTA CTC CAA GAA ATT GGC AAA TTT GAC TCG AAG GAT        2565
366 Ile Thr Lys Glu Leu Leu Gln Glu Ile Gly Lys Phe Asp Ser Lys Asp
367                 245                     250                     255
369 GTC CAC AAC AAT CTT AAC CAG CTT CAA GTC AAA TTG AAG GAA AGT TTG        2613
370 Val His Asn Asn Leu Asn Gln Leu Gln Val Lys Leu Lys Glu Ser Leu
371             260                     265                     270
373 AAG GGA AAG AAG TTC CTT ATT GTT TTG GAT GAT GTG TGG AAT GAA AAT        2661
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375             275                     280                     285
377 TAC AAC GAG TGG AAT GAC TTG AGA AAT ATT TTT GCA CAA GGA GAT ATA        2709
378 Tyr Asn Glu Trp Asn Asp Leu Arg Asn Ile Phe Ala Gln Gly Asp Ile
379         290                     295                     300
381 GGA AGT AAG ATC ATT GTG ACG ACA CGC AAA GAC AGT GTT GCC TTG ATG        2757
382 Gly Ser Lys Ile Ile Val Thr Thr Arg Lys Asp Ser Val Ala Leu Met
383 305                 310                     315                 320
385 ATG GGA AAT GAG CAA ATT CGC ATG GGC AAT TTG TCT ACC GAA GCC TCT        2805
386 Met Gly Asn Glu Gln Ile Arg Met Gly Asn Leu Ser Thr Glu Ala Ser
387             325                     330                     335
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390 Trp Ser Leu Phe Gln Arg His Ala Phe Glu Asn Met Asp Pro Met Gly
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VERIFICATION SUMMARY   DATE: 06/04/2002
PATENT APPLICATION: **US/09/011,307**   TIME: 14:54:04

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L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]